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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Thu Oct 11 14:12:44 EDT 2007

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Application No: 10756153 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-24 13:17:09.961
Finished: 2007-09-24 13:17:12.904
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 943 ms
Total Warnings: 16
Total Errors: 8
No. of SeqIDs Defined: 54
Actual SeqID Count: 54

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (27)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (32)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)

Input Set:

Output Set:

Started: 2007-09-24 13:17:09.961
Finished: 2007-09-24 13:17:12.904
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 943 ms
Total Warnings: 16
Total Errors: 8
No. of SeqIDs Defined: 54
Actual SeqID Count: 54

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)

SEQUENCE LISTING

<110> Johnson, Leslie S.

Li, Hua

Tuailon, Nadine

<120> SOLUBLE FCgammaR FUSION PROTEINS AND METHODS OF USE THEREOF

<130> 11183-005-999

<140> 10756153

<141> 2004-01-13

<141> 2004-01-13

<150> 60/439,709

<151> 2003-01-13

<160> 54

<170> FastSEQ version 4.0

<210> 1

<211> 420

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIa-G2

<400> 1

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1 5 10 15

Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
20 25 30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
35 40 45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
50 55 60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65 70 75 80

Asp	Pro	Val	Gln	Leu	Glu	Val	His	Ile	Gly	Trp	Leu	Leu	Leu	Gln	Ala	85	90	95
Pro	Arg	Trp	Val	Phe	Lys	Glu	Glu	Asp	Pro	Ile	His	Leu	Arg	Cys	His	100	105	110
Ser	Trp	Lys	Asn	Thr	Ala	Leu	His	Lys	Val	Thr	Tyr	Leu	Gln	Asn	Gly	115	120	125
Lys	Gly	Arg	Lys	Tyr	Phe	His	His	Asn	Ser	Asp	Phe	Tyr	Ile	Pro	Lys	130	135	140
Ala	Thr	Leu	Lys	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Arg	Gly	Leu	Val	Gly	145	150	155
Ser	Lys	Asn	Val	Ser	Ser	Glu	Thr	Val	Asn	Ile	Thr	Ile	Thr	Gln	Gly	165	170	175
Leu	Ala	Val	Ser	Thr	Ile	Ser	Ser	Phe	Phe	Pro	Pro	Gly	Tyr	Gln	Val	180	185	190
Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	195	200	205
Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	210	215	220
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	225	230	235
His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Met	Glu	245	250	255
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	260	265	270
Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	275	280	285
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	290	295	300
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	305	310	315
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	325	330	335
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	340	345	350
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	355	360	365
Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr			

370	375	380
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
385	390	395 400
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
	405	410 415
Ser Pro Gly Lys		
	420	
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<212> PRT		
<213> Homo sapiens		
<220>		
<223> sFcRIIb-G2		
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Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr		
	20	25 30
His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu		
	35	40 45
Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn		
	50	55 60
Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp		
65	70	75 80
Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro		
	85	90 95
His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser		
	100	105 110
Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys		
	115	120 125
Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala		
	130	135 140
Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr		
145	150	155 160
Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser		

<223> sFcRIIa(131R)-G2

<400> 3

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser
165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
225 230 235 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
245 250 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

275		280		285
Gly Leu Pro Ala Pro Ile	Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln			
290	295	300		
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met				
305	310	315		320
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro				
	325	330		335
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn				
	340	345		350
Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu				
	355	360		365
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val				
	370	375		380
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln				
385	390	395		400
Lys Ser Leu Ser Leu Ser Pro Gly Lys				
	405			

<210> 4

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIa(131H)-G2

<400> 4

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val			
1	5	10	15
Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro			
	20	25	30
Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr			
	35	40	45
His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly			
	50	55	60
Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His			
65	70	75	80
Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu			

85	90	95
Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp		
100	105	110
Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys		
115	120	125
Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser		
130	135	140
His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe		
145	150	155
Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser		
165	170	175
Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys		
180	185	190
Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys		
195	200	205
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val		
210	215	220
Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr		
225	230	235
Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu		
245	250	255
Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His		
260	265	270
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys		
275	280	285
Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln		
290	295	300
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met		
305	310	315
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro		
325	330	335
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn		
340	345	350
Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu		
355	360	365
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val		
370	375	380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys
405

<210> 5

<211> 1382

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIB insert with signal sequence

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tgactgcaag tccccccagc cttgggggtca tatgcttctg tggacagctg tgctattcct	120
ggctcctgtt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac tcgagcccca	180
gtggatcaac gtgctccagg aggactctgt gactctgaca tgccggggga ctcacagccc	240
tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc acacgcagcc	300
cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc agactggcca	360
gaccagctc agcgaccctg tgcattctgac tgtgctttct gagtggctgg tgctccagac	420
ccctcacctg gagttccagg agggagaaaac catcgtgctg aggtgccaca gctggaagga	480
caagcctctg gtcaagggtca cattcttcca gaatggaaaa tccaagaaat tttcccgttc	540
ggatcccaac ttctccatcc cacaagcaaa ccacagtcac agtggtgatt accactgcac	600
aggaaacata ggctacacgc tgttctcatc caagcctgtg accatcactg tccaagctcc	660
cagctcttca cccatggagg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc	720
acctgtggca ggaccgtcag tcttcttttt cccccaaaa cccaaggaca ccctcatgat	780
ctcccggacc cctgaggtca cgtgcgtggg ggtggacgtg agccacgaag accccgaggt	840
ccagttcaac tgggtacgtg acggcatgga ggtgcataat gccaagacaa agccacggga	900
ggagcagttc aacagcacgt tccgtgtggg cagcgtcttc accgtcgtgc accaggactg	960
gctgaacggc aaggagtaca agtgcaagggt ctccaacaaa ggctcccag ccccatcga	1020

gaaaaccatc	tccaaaacca	aagggcagcc	ccgagaacca	caggtgtaca	ccctgcccc	1080
atccccgggag	gagatgacca	agaaccaggt	cagcctgacc	tgcttggtea	aaggcttcta	1140
ccccagcgac	atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	1200
cacacctccc	atgctggact	ccgacggctc	cttcttcttc	tacagcaagc	tcaccgtgga	1260
caagagcagg	tggcagcagg	ggaacgtctt	ctcatgctct	gtgatgcatg	aggctctgca	1320
caaccactac	acacagaaga	gcctctccct	gtctccgggt	aaatgagtgc	ggccgcgaat	1380
tc						1382

<210> 6

<211> 1418

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIA insert

<400> 6

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gtagcaggct	tgaggtctgg	acatatatat	gggtgacaat	gacatccact	ttgcctttct	120
ctccacaggt	gtccactcca	tcgggactga	agatctcccc	aaggctgtgg	tgttcctgga	180
gcctcaatgg	tacaggggtgc	tcgagaagga	cagtgtgact	ctgaagtgcc	agggagccta	240
ctccccctgag	gacaattcca	cacagtgggt	tcacaatgag	agcctcatct	caagccaggc	300
ctcgagctac	ttcattgacg	ctgccacagt	cgacgacagt	ggagagtaca	ggtgccagac	360
aaacctctcc	accctcagtg	acccggtgca	gctagaagtc	catatcgget	ggctgttget	420
ccaggccccct	cggtgggtgt	tcaaggagga	agaccctatt	cacctgaggt	gtcacagctg	480
gaagaacact	gctctgcata	aggteacata	tttacagaat	ggcaaaggca	ggaagtattt	540
tcatcataat	tctgacttct	acattccaaa	agccacactc	aaagacagcg	gtcctacttt	600
ctgcagggggg	cttggtggga	gtaaaaatgt	gtcttcagag	actgtgaaca	tcaccatcac	660
tcaagggtttg	gcagtgtcaa	ccatctcatc	attctttcca	cctgggtacc	aagtcgagcg	720
caaatgttgt	gtcgagtgcc	caccgtgccc	agcaccacct	gtggcaggac	cgtcagtctt	780
cctcttcccc	ccaaaacca	aggacaccct	catgatctcc	cggacccttg	aggtcacgtg	840

cgtggtggtg gacgtgagcc acgaagaccc cgaggccag ttcaactggt acgtggacgg

9